

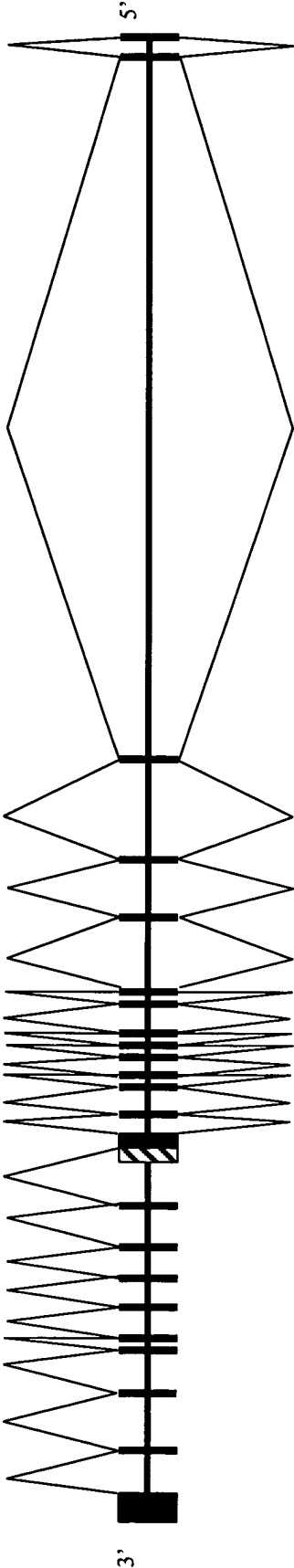
FIG. 1

A) T2DM-1

Exons:

23 22 21 20 19 18 17 16 15 14 13 12 - 8 7 6 5 4 3 2 1

T2DM-1a

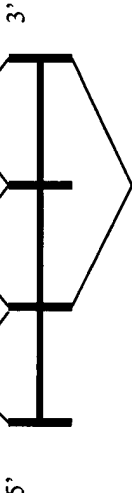


B) T2DM-2

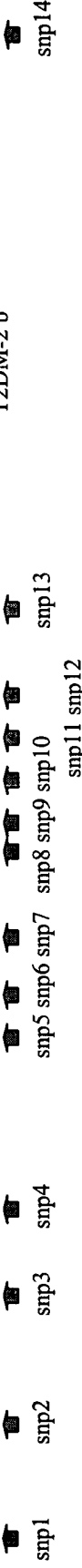
Exons:

1 2 3 4

T2DM-2a



C) SNP Map



**T2DM-1a:** 4211 basepairs (long form, exons 1-24) (SEQ ID NO:1)

AAATCAGATGCTCTGTGATTAATCGTGGAGGATTACAGGACACGACCACAAACGCTGCCAGATAAGAGTCC  
CGGCTGCATTATCAGAGCCCCGGCAGGGCACCGGCCCTCCCTGCACCAGAAGGAAGACTCGGGGCGCAGCAG  
GTCCTCAAGGCATCTTCCCAGAGAGCGGGACCAGCGGCTGGTGGCCAGTGTGGATGGAATTTGCAGAGC  
CCTAGCTCGAGTCCGGGAGTCCCGGGCCAGATGGGAGCAGACGCTTGCTGGCGGCAATAGGGAAAGTGAG  
GCAGCTGCAAGGAGGGCGGGGGACTGCACTCGAGTGTCCAGACCTGCTCGATGGTGACCACCATGTCCG  
TGAGGTTGCGGTTCTGTCCCTGGGGACACAGGGGCCGTGGGGGTCTGGGCCGGAGCGCCTCCTTCGC  
AGGCTTCAGCAGTGCACAGAGCCGGAGGATCGCAAAGTCCATCAACAGGAACCTCCGTGAGATCGCGAATG  
CCTGCAAAATCCTCCAAGATGTACGGCAGCTGCGGAAGGGGTCTGGTCTGTGCAGACCCGAAGCCCCAGC  
AGGTGAAGAAGATCTTCAAGCATTGAAAAGAGGCCTCAAGGAGTATCTGTGTGTGCAGCAGGCTGAGCT  
GGACCACCTGTCTGGACGCCACAAAGACACCAGGAGGAATTCCAGGCTGGCTTTCTATTATGACCTGGAC  
AAGCAAACGCGCTGTGTGGAAAGGCACATTTCGAAGATGGAGTTTCACATCAGCAAGGTGGATGAGCTGT  
ACGAGGACTACTGCATCCAGTGCCGCCTGCGCGACGGCGCCTCCAGCATGCAGCGGGCCTTCGCCCCGTG  
CCCCCGAGCCGCGCAGCCCCGAGAGACCTGCAGGAGCTGGGCCGACGCTGCACGAGTGCGCCGAGGAC  
ATGTGGCTCATCGAGGGGGCCCTGGAGGTTACCTGGGCGAGTTCCACATCAGGATGAAAGGCTTGGTGG  
GCTACGCACGCCTCTGTCCCGAGACCACTATGAGGTGCTCATGCGTCTGGGCCGCCAGCGTTGGAAGCT  
CAAGGGTCGGATCGAGTCAGATGACAGCCAGACCTGGGACGAAGAGGAGAAGGCCTTCATCCCCACGCTG  
CATGAGAACCTGGACATCAAGGTGACGGAGTTGCGGGGCCCTGGGCTCGCTGGCTGTGGGTGCAGTGACGT  
GTGACATCGCCGACTTCTTCACGACGCGGCCGACGGTTCATCGTGGTGGACATCACGGAGTTGGGTACCAT  
CAAGCTGCAGCTGGAGGTGCAGTGGAACCCGTTTGATACTGAGAGCTTCCTGGTGTACCCAGCCCCACG  
GGCAAGTTTTCTATGGGCAGCAGGAAGGGCTCCTTGTAACACTGGACACCCCCGAGCACCCCCAGCTTCC  
GGGAGAGATACTACCTGTCTGTCTACAGCAGCCAACACAGCAGGCCTTGCTGCTGGGTGGCCCAAGGGC  
CACCTCCATCCTCAGCTACCTGTCTGACAGCGACCTCCGGGGTCCCAGCCTAAGAAGCCAGAGTCAGGAG  
CTGCCTGAGATGGACTCCTTCAGCTCTGAGGACCCCCGAGACACGGAGACCAGCACGTCGGCGTCCACCT  
CAGATGTGGGCTTCCTGCCCTTGACCTTCGGTCCCCACGCCTCCATTGAAGAGGAGGCTCGGGAGGACCC  
CCTGCCCCCAGGTCTCCTGCCAGAGATGGCCACCTCTCTGGAGGCCCGTTTGCAGAGCAGCCTGGCTGG  
AGGAACTTAGGAGGGGAGAGCCCCAGCCTGCCACAGGGGCTCCCTGTTCCACAGCGGCACAGCCTCGAGTA  
GCCAGAACGGCCACGAGGAAGGGGCAACCGGGGACAGAGAGGACGGGCCTGGCGTGGCCCTCGAGGGGCC  
TCTGCAGGAGGTCTTGAGTTGCTGAGGCCCACGGACTCCACCCAGCCCCAGCTCCGGGAGCTGGAGTAC  
CAGGTCTCTGGCTTCCGGGACCGGCTGAAGCCCTGCAGAGCACGGCAGGAGCACACCTCGGCCGAGAGCC  
TGATGGAGTGCATCCTGGAGAGCTTCGCCTTCCTCAATGCCGACTTCGCCCTGGATGAGCTGTCCCTGTT  
TGGGGGCTCCCAGGGTCTCCGAAAGGACCGGGCCCTGCCCCACCGTCATCACTGAAAGCGTCATCCAGG  
GAACTCACAGCCGGTGCCCCAGAGCTGGACGTGCTGCTGATGGTACACCTCCAAGTCTGCAAAGCTCTGC  
TGCAGAACTGGCCTCCCCTAATTTATCAAGGCTGGTCCAGGAATGCCTCCTGGAAGAAGTGGCACAGCA  
AAAGCACGTTCTGGAGACACTTTCTGTCTTGACTTTGAGAAGGTTCGGCAAGGCAACATCCATTGAAGAG  
ATCATCCACAGGCCTCGCGGACGAAGGGGTGCCTGAAGCTGTGGAGAGGGTGCACAGGGCCTGGCAGGG  
TCCTGTCTGCCCTGCCACGACGTGCTGAACAGCTCAAGAAAACCTTCAGCACAGAGTCAGAGGGAA  
GTACCCAGGACAGCTGGAAATAGCGTGCCGACGGCTCCTGGAGCAGGTGGTCAGCTGTGGTGGGCTGCTC  
CCCGGAGCTGGGCTCCCAGAAGAACAGATCATTACCTGGTTCCAGTTTCACAGCTACCTGCAGAGGCAGA  
GCGTCTCTGACCTGGAGAAGCACTTCACCCAGCTCACCAAGGAAGTGACACTCATCGAGGAGCTTCACTG  
TGCGGGACAGGCCAAGGTGGTCCGGAAGCTGCAGGGGAAGCGGCTGGGCCAGCTCCAGCCTCTGCCCCAG  
ACCTTAAGAGCCTGGGCGCTGCTCCAGCTGGACGGCACTCCGAGGGTGTGCAGGGCGGCCAGCGCTCGCC  
TGGCTGGTGCAGTCAGGAACAGAAGCTTCGGGAAAAGGCTTTGCTGTCTACACCAACGCCCTGGCAGA  
GAACGACGCAAGGCTCCAGCAGGCCGCATGCCTAGCGCTCAAACACCTCAAGGGCATTGAAAGCATCGAC  
CAGACTGCCAGCCTGTGCCAGTCTGACCTGGAGGCCGTGCGGGCGGCAGCCCGGAAACCACACTGTCGT  
TCGGTGAAAAAGGACGGTTAGCTTTTGAGAAGATGGACAAGCTCTGCTCAGAACAAAGAGAAGTCTTTTG  
CCAGGAGGCAGATGTTGAAATCACAATATTTTAAAAAATCCTGGCTGATGAGCACAATCTCACATCGTT  
TTTTTTGCTGCTGCCAGCCTGGACATAGCCTGCACTCTGGGTAATGGTGCTGTGCACTCCTCCAGGAGT  
GTGAGCTGCCAGAGCTCTACCTGAGACTCCGGCCATTGACCCAGCCCCAGGGCATGGGCTGGTCTTTTG  
TACAGAGGCAGAAAAAGCAAGGCAAAGGTACAGCATTCCAGGGGCTGCACGGCCTCAACAGAGCGCTCA  
ACTTCTGGCTGAGGGTCTGTGTGACCTTCCCCGAGATGCAGAGCTGAGCCAACTAGGTGGCCACCTACA

FIG. 2 A

AAAGGGCCAAGGCCAGGCAAGTTGAGGCCCTAAATAAAAGGCTCCAAGGCAAGTGTGTAGAACTCCAGGC  
 CTCGCTGCCGGTCAGCTGCTCGGCACTTCTGCGTCAAGAGGCACTGGGGATGCAGCAGGCTGGCAGGTGG  
 CTGGCCCTGCTAATGCAAGACTGCTCAGGCCATTTTCAGCAGCAGCCAGGTGTCACCTTGGTGAGCTGGGG  
 AAGGTGGGAAGGCACAAAGCCAGGGTTTCTACAACCACACTCTCAGCCCGACTGACTTGCTGCGAGTGCT  
 GGTGGAGCTCACAGACGGCGGCTGGTGGATGGTGGACTGTGAACCTCACTTTCCCTATGTTTCAGCAGCAC  
 AAAGGGAAGAAGCCACCACATCAGCCCAGGAGCCCTGAGCAGCACAGGCAGTAGGGCCACTCACTTTGGC  
 CATCCGCACCCAAATGCAATCAATCAACCCAGCTTCGGAAGCTACCCTAGGATCTCGTCAATAAACTGCT  
 AAGAAGCCATCAACTGGCCTAAAGAAAGAGTTCACTGAAGAACGCAATTGCTTTAAAGAAAGAAAATTA  
 GTTTCCTATTTAAGTCTTAAAAAAAAGCAAACCATGTCCTGAGATGTCTGTGTTAATAGTGCAGAGAGAA  
 CCTAGGGTTTGAGGTTGCTGTAGCAATGGCATTGGAGAACTTTAACTTGAACATTCTCATCGATACTTCC  
 TGGACATATTT

**T2DM-1a: 946 amino acids (long form, exons 1-24) (SEQ ID NO:2)**

M S V R L R F L S P G D T G A V G V V G R S A S F A G F S S A Q S R R  
 I A K S I N R N S V R S R M P A K S S K M Y G T L R K G S V C A D P K  
 P Q Q V K K I F E A L K R G L K E Y L C V Q Q A E L D H L S G R H K D  
 T R R N S R L A F Y Y D L D K Q T R C V E R H I R K M E F H I S K V D  
 E L Y E D Y C I Q C R L R D G A S S M Q R A F A R C P P S R A A R E S  
 L Q E L G R S L H E C A E D M W L I E G A L E V H L G E F H I R M K G  
 L V G Y A R L C P G D H Y E V L M R L G R Q R W K L K G R I E S D D S  
 Q T W D E E E K A F I P T L H E N L D I K V T E L R G L G S L A V G A  
 V T C D I A D F F T T R P Q V I V V D I T E L G T I K L Q L E V Q W N  
 P F D T E S F L V S P S P T G K F S M G S R K G S L Y N W T P P S T P  
 S F R E R Y Y L S V L Q Q P T Q Q A L L L G G P R A T S I L S Y L S D  
 S D L R G P S L R S Q S Q E L P E M D S F S S E D P R D T E T S T S A  
 S T S D V G F L P L T F G P H A S I E E E A R E D P L P P G L L P E M  
 A H L S G G P F A E Q P G W R N L G G E S P S L P Q G S L F H S G T A  
 S S S Q N G H E E G A T G D R E D G P G V A L E G P L Q E V L E L L R  
 P T D S T Q P Q L R E L E Y Q V L G F R D R L K P C R A R Q E H T S A  
 E S L M E C I L E S F A F L N A D F A L D E L S L F G G S Q G L R K D  
 R P L P P P S S L K A S S R E L T A G A P E L D V L L M V H L Q V C K  
 A L L Q K L A S P N L S R L V Q E C L L E E V A Q Q K H V L E T L S V  
 L D F E K V G K A T S I E E I I P Q A S R T K G C L K L W R G C T G P  
 G R V L S C P A T T L L N Q L K K T F Q H R V R G K Y P G Q L E I A C  
 R R L L E Q V V S C G G L L P G A G L P E E Q I I T W F Q F H S Y L Q  
 R Q S V S D L E K H F T Q L T K E V T L I E E L H C A G Q A K V V R K  
 L Q G K R L G Q L Q P L P Q T L R A W A L L Q L D G T P R V C R A A S  
 A R L A G A V R N R S F R E K A L L F Y T N A L A E N D A R L Q Q A A  
 C L A L K H L K G I E S I D Q T A S L C Q S D L E A V R A A A R E T T  
 L S F G E K G R L A F E K M D K L C S E Q R E V F C Q E A D V E I T I  
 F\*

**T2DM-1b: 2278 basepairs (short form, exons 1-14) (SEQ ID NO:3)**

AAATCAGATGCTCTGTGATTAATCGTGGAGGATTACAGGACACGACCAAACGCTGCCAGATAAGAGTCC  
 CGGCTGCATTATCAGAGCCCGGCAGGGCACCGGCCTCCCTGCACCAGAAGGAAGACTCGGGGCGCAGCAG  
 GTCCTCAAGCGATCTTCCCAGAGAGCGGGACCAGCGGCTGGTGGCCAGTGTGGATGGAATTTGCAGAGC  
 CCTAGCTCGAGTCCGGGAGTCCCGGGCCAGATGGGAGCAGACGCTTGCTGGCGGCAATAGGGAAAGTGAG  
 GCAGCTGCAAGGAGGGCGGGGACTGCACTCGAGTGTCCAGACCTGCTCGATGGTGACCACCATGTCCG  
 TGAGGTTGCGGTTCTGTCCCCTGGGGACACAGGGGCCGTGGGGGTCTGGGGCCGGAGCGCCTCCTTCGC

**FIG. 2 B**

AGGCTTCAGCAGTGCACAGAGCCGGAGGATCGCAAAGTCCATCAACAGGAACTCCGTGAGATCGCGAATG  
 CCTGCAAAATCCTCCAAGATGTACGGCACGCTGCGGAAGGGGTCTGGTCTGTGCAGACCCGAAGCCCCAGC  
 AGGTGAAGAAGATCTTCAAGCATTGAAAAGAGGCCTCAAGGAGTATCTGTGTGTGCAGCAGGCTGAGCT  
 GGACCACCTGTCTGGACGCCACAAAGACACCAGGAGGAATTCCAGGCTGGCTTTCTATTATGACCTGGAC  
 AAGCAAACGCGCTGTGTGGAAAGGCACATTTCGGAAGATGGAGTTTCACATCAGCAAGGTGGATGAGCTGT  
 ACGAGGACTACTGCATCCAGTGCCGCCTGCGCGACGGCGCCTCCAGCATGCAGCGGGCCTTCGCCCCGGTG  
 CCCCCCGAGCCGCGCAGCCCCGAGAGAGCCTGCAGGAGCTGGGCGCAGCCTGCACGAGTGCGCCGAGGAC  
 ATGTGGCTCATCGAGGGGGCCCTGGAGGTTACCTGGGCGAGTTCCACATCAGGATGAAAGGCTTGGTGG  
 GCTACGCACGCCTCTGTCCCGGAGACCACTATGAGGTGCTCATGCGTCTGGGCGGCCAGCGTTGGAAGCT  
 CAAGGGTCGGATCGAGTCAGATGACAGCCAGACCTGGGACGAAGAGGAGAAGGCCTTCATCCCCACGCTG  
 CATGAGAACCTGGACATCAAGGTGACGGAGTTGCGGGGCCTGGGCTCGCTGGCTGTGGGTGCAGTGACGT  
 GTGACATCGCCGACTTCTTACGACGCGGCCGAGGTCATCGTGGTGGACATCACGGAGTTGGGTACCAT  
 CAAGCTGCAGCTGGAGGTGCAGTGGAACCCGTTTGATACTGAGAGCTTCCTGGTGTACCCAGCCCCACG  
 GGCAAGTTTTCTATGGGCAGCAGGAAGGGCTCCTTGTACAACAGGACACCCCGAGCACCCCCAGCTTCC  
 GGGAGAGATACTACCTGTCTGTCTACAGCAGCCAACACAGCAGGCCTTGCTGCTGGGTGGCCCAAGGGC  
 CACCTCCATCCTCAGCTACCTGTCTGACAGCGACCTCCGGGGTCCCAGCCTAAGAAGCCAGAGTCAGGAG  
 CTGCCTGAGATGGACTCCTTCAGCTCTGAGGACCCCGAGACACGGAGACCAGCACGTCGGCGTCCACCT  
 CAGATGTGGGCTTCCTGCCCTTGACCTTCGGTCCCCACGCCTCCATTGAAGAGGAGGCTCGGGAGGACCC  
 CCTGCCCCCAGGTCTCCTGCCAGAGATGGCCCACCTCTCTGGAGGGCCGTTTGCAGAGCAGCCTGGCTGG  
 AGGAACTTAGGAGGGGAGAGCCCCAGCCTGCCACAGGGCTCCCTGTTCCACAGCGGCACAGCCTCGAGTA  
 GCCAGAACGGCCACGAGGAAGGGGCAACCGGGGACAGAGAGGACGGGCCTGGCGTGGCCCTCGAGGGGCC  
 TCTGCAGGAGGTCCTGGAGTTGCTGAGGCCCACGGACTCCACCCAGCCCCAGCTCCGGGAGCTGGAGTAC  
 CAGGTCCTCGGCTTCCGGGACCGGCTGAAGGTATGGCCACCCCGCCCCGGGCGGTGGCCCTGCTTTGCTG  
 ATGGCATGATGACTGGGAGTCGGGGGCTCTGGGGCCACGCAGCCTGGGCGACATCCTGGCCTCACCTCT  
 GCGTGACCTGGGTGGGCCGTGTCTCTCTGGGCCTTGGTTTCCTCATCTGGCAAGCGGGGATAACAACAGC  
 CCTCATGGGGCTCAGGAAGATTTTAAGAGTTACAGTAGATAGGCTCATGCACATCCAGCCAGAACTGG  
 CCCCATCTCGCACCTTCTGACCTGGGTGGGCGGGGCTG

**T2DM-1b:** 625 amino acids (short form, exons 1-14) (SEQ ID NO:4)

M S V R L R F L S P G D T G A V G V V G R S A S F A G F S S A Q S R R  
 I A K S I N R N S V R S R M P A K S S K M Y G T L R K G S V C A D P K  
 P Q Q V K K I F E A L K R G L K E Y L C V Q Q A E L D H L S G R H K D  
 T R R N S R L A F Y Y D L D K Q T R C V E R H I R K M E F H I S K V D  
 E L Y E D Y C I Q C R L R D G A S S M Q R A F A R C P P S R A A R E S  
 L Q E L G R S L H E C A E D M W L I E G A L E V H L G E F H I R M K G  
 L V G Y A R L C P G D H Y E V L M R L G R Q R W K L K G R I E S D D S  
 Q T W D E E E K A F I P T L H E N L D I K V T E L R G L G S L A V G A  
 V T C D I A D F F T T R P Q V I V V D I T E L G T I K L Q L E V Q W N  
 P F D T E S F L V S P S P T G K F S M G S R K G S L Y N W T P P S T P  
 S F R E R Y Y L S V L Q Q P T Q Q A L L L G G P R A T S I L S Y L S D  
 S D L R G P S L R S Q S Q E L P E M D S F S S E D P R D T E T S T S A  
 S T S D V G F L P L T F G P H A S I E E E A R E D P L P P G L L P E M  
 A H L S G G P F A E Q P G W R N L G G E S P S L P Q G S L F H S G T A  
 S S S Q N G H E E G A T G D R E D G P G V A L E G P L Q E V L E L L R  
 P T D S T Q P Q L R E L E Y Q V L G F R D R L K V W P P R P G R W P C  
 F A D G M M T G S R G L W G H A A W A D I L A S P L R D L G G P C L S  
 G P W F P H L A S G D N N S P H G A Q E D F K S S Q

FIG. 2 C

**T2DM-2a:** 828 basepairs (long form, exons 1-4) (SEQ ID NO:5)

GGAGAGGAAGCCAGATGCTCCCAGACACTGGGGACTGTCCTGGGCCTCCGTCCCCAAGGTGTGGCTGGAGG  
AAGCAGAGTCTACTCCCGCTAAGTCTGTCCGCTCACTGCTGGCCAAAGCTGCCCTGCGTCTCCTCCCCACC  
GCCAGCCAGAGGGAACCTGCAATTTACCTCATTTAGAGCATCCGGAGCCCAGGACTGCTCAGTCAACCCCT  
CTGGAATGCCCACAACCTCCCCACAGGCCAGCCGGCCTTGGGACTCCCGCACAGCCACGTGAGCCGGTGGAG  
CCGGGTCTGTTTGCTAGTGGAGGCTGTTAACAGCACGGGAAGTGGTCAAGGGTTCAACAAGAGATGAGCCA  
TCTGGTCTCCAGAGGTTGTGACTTCAATATACCCTCTCATGAGACCTTTCCTGGCCCCCTTATCTGTGGAG  
GAGGCACGTGACCCACATGGTCTGGCCACTGATGACTGAACAAGCTATGGACACCGGACCCCGGAGAGACC  
ATTCACTCACTGGCCACGAACATGAGTTCAGATACATGCCCCAAAAGGATGAGCCTGGGTACTGGATTCCC  
TCCCTCAGAAACGTGAATCAAGAGACACAGGATGTTCTGTGGTCCAGATACTTGAGCTAAAAGGTGATG  
GATACCTGGATGTGGGGTGGTCATTCTGGGGAGTACGTCCATATAGAAAGAGGAGCAGGTGCTGTGGGATT  
CTGGATCCCAGTGATAGAGCTAAGTGGCTGGATCAAGCTTCACCTGAAACCCACTCTACTTGTCTTAGTCC  
ATTTTGTGTTGCTATAAAAGAATACCTGCAACTGGGTAATGTATAAA

**T2DM-2b:** 597 basepairs (short form, exons 2 & 4) (SEQ ID NO:6)

CATCCGGAGCCCAGGACTGCTCAGTCAACCCCTCTGGAATGCCCACAACCTCCCCACAGGCCAGCCGGCCTTG  
GACTCCCGCACAGCCACGTGAGCCGGTGGAGCCGGGTCTGTTTGCTAGTGGAGGCTGTTAACAGCACGGG  
AAGTGGTCAAGGGTTCAACAAGAGATGAGCCATCTGGTCTCCAGAGGTGGAGGAGGCACGTGACCCACAT  
GGTCTGGCCACTGATGACTGAACAAGCTATGGACACCGGACCCCGGAGAGACCATTCACTCACTGGCCACG  
AACATGAGTTCAGATACATGCCCCAAAAGGATGAGCCTGGGTACTGGATTCCCTCCCTCAGAAACGTGAAT  
CAAGAGACACAGGATGTTCTGTGGTCCAGATACTTGAGCTAAAAGGTGATGGATACCTGGATGTGGGGT  
GGTCATTCTGGGGAGTACGTCCATATAGAAAGAGGAGCAGGTGCTGTGGGATTCTGGATCCCAGTGATAGA  
GCTAAGTGGCTGGATCAAGCTTCACCTGAAACCCACTCTACTTGTCTTAGTCCATTTTGTGTTGCTATAAA  
AGAATACCTGCAACTGGGTAATGTATAAA

FIG. 2 D

**Gene Organization:**

T2DM-1a				
Exon	Begins cDNA	Ends cDNA	Begins Genomic*	Ends Genomic*
1	1	55	49036730	49036676
2	56	334	49036419	49036141
3	335	453	48975871	48975753
4	454	600	48965147	48965001
5	601	679	48961095	48961017
6	680	703	48956219	48956196
7	704	757	48955921	48955868
8	758	907	48954737	48954588
9	908	971	48954371	48954308
10	972	1141	48953970	48953628
12	1142	1287	48953549	48953404
13	1288	1417	48949789	48949660
14	1418	1990	48947659	48947087
15	1991	2121	48942725	48942595
16	2122	2245	48941278	48941155
17	2246	2381	48940519	48940384
18	2382	2543	48939729	48939568
19	2544	2705	48938211	48938050
20	2706	2908	48937561	48937359
21	2909	2992	48934784	48934701
22	2993	3083	48932907	48932817
23	3084	4211	48932347	48931220

\*Genomic positions correspond to the Build 29 human genome assembly from NCBI (UCSC versoin hg11)

**FIG. 3 A**

T2DM-1b				
Exon	Begins cDNA	Ends cDNA	Begins Genomic*	Ends Genomic*
1	1	55	49036730	49036676
2	56	334	49036419	49036141
3	335	453	48975871	48975753
4	454	600	48965147	48965001
5	601	679	48961095	48961017
6	680	703	48956219	48956196
7	704	757	48955921	48955868
8	758	907	48954737	48954588
9	908	971	48954371	48954308
10	972	1141	48953970	48953628
12	1142	1287	48953549	48953404
13	1288	1417	48949789	48949660
14	1418	2278	48947659	48946799

\*Genomic positions correspond to the Build 29 human genome assembly from NCBI (UCSC version hg11)

**FIG. 3 B**

**Gene Organization:**

T2DM-2a				
Exon	Begins cDNA	Ends cDNA	Begins Genomic*	Ends Genomic*
1	1	181	48981701	48981881
2	182	370	48990713	48990901
3	371	420	48998961	48999010
4	421	828	49004881	49005288

\*Genomic positions correspond to the Build 29 human genome assembly from NCBI (UCSC version hg11)

T2DM-2b				
Exon	Begins cDNA	Ends cDNA	Begins Genomic*	Ends Genomic*
1	1	189	48990713	48990901
2	190	597	49004881	49005288

\*Genomic positions correspond to the Build 29 human genome assembly from NCBI (UCSC version hg11)

**FIG. 3 C**



**SNP1**

**-TTGA (IN/DEL)**

TCAAACCCTAGGTTCTCTCTGCACTATTAACACAGACATCTCAGGACATGGTTTGCTTT  
TTTTTAAGACTTAAATAGGAACTAATTTTTCTTTCTTTAAAGCAATTGCGTTCTTCAG  
TGAAC TCTTTCTTTAGGCCAGTTGATGGCTTCTTAGCAGTTTATTGACGAGATCCTAGG  
GTAGCTTCCGAAGCTGGGTTGATTGATTGCATTTGGGTGCGGATGGCCAAAGTGAGTGG  
CCCTACTGCCTGTGCTGCTCAGGGCTCCTGGGCTGATGTGGTGGCTTCTTCCCTTTGTG  
CTGCTGAACATAGGGAAAGTGAGGTTACAGTCCACCATCCACCAGCCGCCGTCTGTGA  
GCTCCACCAGCACTCGCAGCAAGTCAGTCGGGCTGAGAGTGTGGTTGTA (SEQ ID  
NO: 9)

TCAAACCCTAGGTTCTCTCTGCACTATTAACACAGACATCTCAGGACATGGTTTGCTTT  
TTTTTAAGACTTAAATAGGAACTAATTTTTCTTTCTTTAAAGCAATTGCGTTCTTCAG  
TGAAC TCTTTCTTTAGGCCAGTTGATGGCTTCTTAGCAGTTTATTGACGAGATCCTAGG  
GTAGCTTCCGAAGCTGGGTTGATTGCATTTGGGTGCGGATGGCCAAAGTGAGTGGCCCT  
ACTGCCTGTGCTGCTCAGGGCTCCTGGGCTGATGTGGTGGCTTCTTCCCTTTGTGCTGC  
TGAACATAGGGAAAGTGAGGTTACAGTCCACCATCCACCAGCCGCCGTCTGTGAGCTC  
CACCAGCACTCGCAGCAAGTCAGTCGGGCTGAGAGTGTGGTTGTA (SEQ ID  
NO: 10)

**SNP2**

**A/G**

CCTAACCAGCTTCTCCTCTTAGAATTTCTGCTGATCCATCCCAGAATGAATGGGAGTT  
CAATCTGTACTGAATTATCTTTTCATCTAGCAATTGTGCAATTCCAAATGCAGGTGAGGT  
TGAGGGAAAGCGGGCATCCCCTCACATCCATGGGATCTATGTGTGGGTTGTATCAAGAG  
TCTCAAAAATGCTCATATTCTCCAGTCCTAGAATTGGGTCTAGCCTAAGGAAATAATTC  
AGAACTCCATGTTTTTTTTAAAGCTTTATGCACAAACATGATCATAAGACATGATTTATG  
ATAAAAATTGGATGAAGTAACTTTCTATGAAAGCAGCTGAGTAGGTTAAATTAAGGT  
ATACACTTGATAGCCCCTTCATAAAGAATTCTCAAGTGAAAAAAAAA (SEQ ID  
NO: 11)

CCTAACCAGCTTCTCCTCTTAGAATTTCTGCTGATCCATCCCAGAATGAATGGGAGTT  
CAATCTGTACTGAATTATCTTTTCATCTAGCAATTGTGCAATTCCAAATGCAGGTGAGGT  
TGAGGGAAAGCGGGCATCCCCTCACATCCATGGGATCTATGTGTGGGTTGTATCAAGAG  
TCTCAAAAATGCTCATATTCTCCGGTCCTAGAATTGGGTCTAGCCTAAGGAAATAATTC

**FIG. 4 A**

AGAACTCCATGTTTTTTTAAAGCTTTATGCACAAACATGATCATAAGACATGATTTATG  
ATAAAAATTGGATGAAGTAAACTTTTCCTATGAAAGCAGCTGAGTAGGTAAATTAAGGT  
ATACACTTGATAGCCCCTTCATAAAGAATTCTCAAGTGAAAAAAAAA (SEQ ID  
NO:12)

**SNP3**

**A/G**

CACCTGCAGTCCCCACAACAACCTGGGAGGGGCTGCTGTCACCAGCCTCTCCTTACAGA  
CAAGGAACCTGGCCTTCTGAGGGGAGGTCCCACGGGGCAGAGGCACAGCTGGGATCACA  
GCTACTGTTTGACGGCACATTCTGCACCTTGAATGTGGCCTGGGGTTACCTCACTGAAC  
CCCGTGCAGTGCCCTCCTCCTATACAGATAGGGAAGCAGAGGCTCAGAGATGTGAATCA  
TTTGCCTAGAGTCACACAGCTGACTGAAGAGTGTGCTGCAACTCCAGGACTTGTCTCCC  
TTACCTCCCCACAAAGAGTGTGTATCTCTGAGCCCAGCCCAGCCACAGCCTCCACTCTG  
GGCCCCGATTAACTCTGGCTATTAGGAAGGCAGAAGAGGCTCCCCGA (SEQ ID  
NO:13)

CACCTGCAGTCCCCACAACAACCTGGGAGGGGCTGCTGTCACCAGCCTCTCCTTACAGA  
CAAGGAACCTGGCCTTCTGAGGGGAGGTCCCACGGGGCAGAGGCACAGCTGGGATCACA  
GCTACTGTTTGACGGCACATTCTGCACCTTGAATGTGGCCTGGGGTTACCTCACTGAAC  
CCCGTGCAGTGCCCTCCTCCTATGCAGATAGGGAAGCAGAGGCTCAGAGATGTGAATCA  
TTTGCCTAGAGTCACACAGCTGACTGAAGAGTGTGCTGCAACTCCAGGACTTGTCTCCC  
TTACCTCCCCACAAAGAGTGTGTATCTCTGAGCCCAGCCCAGCCACAGCCTCCACTCTG  
GGCCCCGATTAACTCTGGCTATTAGGAAGGCAGAAGAGGCTCCCCGA (SEQ ID  
NO:14)

**SNP4**

**A/G**

ATGTGCGGGGATGGCATGGGGAAGGGTGACGATAGAGTGACAAGAGCTGAGCCAAGGA  
CAGTGGGAGAAACAGACGGGGAGGCTGGCAGGAAACGTGGAGCTCGGGTCACCCGGTGG  
GAGTGGTGGCCACTGGGTCACTGCTGGAAGGAGGTGCACTACCGGAGACCCTGGGAGC  
CCCCAAACAGGGACAGCTCATCCAGGGCGAAGTCGGCATTGAGGAAGGCGAAGCTCTCC  
AGGATGCACTCCATCAGGCTCTCGGCCGAGGTGTGCTCCTGCCGTGCTCTGCAGGGCTG  
TGGACGAAGTGGCCAGACCTGAGGGCAACACCGGGCCCCACCCACCCGACTGGGACACT  
GGCCAGGGGCTCACGGCAGACTTGGGCAATGTCCCGGTCCCAAGCC (SEQ ID  
NO:15)

**FIG. 4 B**

ATGTGCGGGGATGGCATGGGGAAGGGTGACGATAGAGTGACAAGAGCTGAGCCAAGGA  
CAGTGGGAGAAACAGACGGGGAGGCTGGCAGGAAACGTGGAGCTCGGGTCACCCGGTGG  
GAGTGGTGGCCACTGGGTCACTGCTGGAAGGAGGTGCACTACCGGAGACCCTGGGAGC  
CCCCAAACAGGGACAGCTCATCCGGGGCGAAGTCGGCATTGAGGAAGGCGAAGCTCTCC  
AGGATGCACTCCATCAGGCTCTCGGCCGAGGTGTGCTCCTGCCGTGCTCTGCAGGGCTG  
TGGACGAAGTGGCCAGACCTGAGGGCAACACCGGGCCCCACCCACCCGACTGGGACACT  
GGCCAGGGGCTCACGGCAGACTTGGGCAATGTCCCGGTCCCAAGCC (SEQ ID  
NO:16)

**SNP5**

**A/C**

GCCAATTCCCGTGCCCCTCAGCAGAAGTCTCAGGGCCTCCAGAAAGGCCTCCGCCCACC  
CCCTCTCAGCCCTGTTACCTTTCATCCTGATGTGGAACTCGCCCAGGTGAACCTCCAGG  
GCCCCCTCGATGAGCCACATGTCCTGCAAAGCCCCGGAGGTGGCTCAGCTGGCTGCCTG  
GGGCTAGGCCACGAGGGCCTCTAACCATCCCTGCAGCCAGACAGAGGCCACAGGCAGAG  
AGACGCCTCCTTGGGGCCCAGAACACCTCCTCCAGCCCCCACTGGCCCAGCTCTCGATG  
TCCCCACTGCCCCGGCCCAGCTCTTGCTGCCCCCTGCTGCCCAGCCCAGCTTGGCCCCGGCC  
CACCTCGGCGCACTCGTGCAGGCTGCGGGCCCAGCTCCTGCAGGCTCT (SEQ ID  
NO:17)

GCCAATTCCCGTGCCCCTCAGCAGAAGTCTCAGGGCCTCCAGAAAGGCCTCCGCCCACC  
CCCTCTCAGCCCTGTTACCTTTCATCCTGATGTGGAACTCGCCCAGGTGAACCTCCAGG  
GCCCCCTCGATGAGCCACATGTCCTGCAAAGCCCCGGAGGTGGCTCAGCTGGCTGCCTG  
GGGCTAGGCCACGAGGGCCTCTAACCATCCCTGCAGCCAGACAGAGGCCACAGGCAGAG  
AGACGCCTCCTTGGGGCCCAGAACACCTCCTCCAGCCCCCACTGGCCCAGCTCTCGATG  
TCCCCACTGCCCCGGCCCAGCTCTTGCTGCCCCCTGCTGCCCAGCCCAGCTTGGCCCCGGCC  
CACCTCGGCGCACTCGTGCAGGCTGCGGGCCCAGCTCCTGCAGGCTCT (SEQ ID  
NO:18)

**SNP6**

**-TTAGTGCCGGGCGCGC (IN/DEL)**

CACTGCCCCACCCACCCCTGCAACATCCACGAGCCAGCTGACCTTGCTGATGTGAAACT  
CCATCTTCCGAATGTGCCTTTCCACACAGCGCGTTTGCTTCTCCCGGAAAAAGGGAAGA  
TGTTTGCAAAGTTGCCTGGGCCACCCACCTGCCCCGCTTGCCCCTGCCACCCTCCTACA  
GGTCCTAACTCAGAGAATGGGGCTTAGTGCCGGGCGCGCCCTCACCATCCCTGAGGAA  
GGCTCATCGCAGAGACTCAGCCTTCCCATTCCTAAATGGGGAGGAGACCCAGGTTTTTC  
TGCCCATCAGGCAGCCAGGAAGATGCAATGAGGCACAGTCATTCTCATCCAGCCAGGCC

**FIG. 4 C**

CAGCCCACCTCACTCACCGTATGCAGACTCACCTTGTCCAGGTCATAATAGAAAGCCTG  
TGA (SEQ ID NO:19)

CACTGCCCCACCCACCCCTGCAACATCCACGAGCCAGCTGACCTTGCTGATGTGAAACT  
CCATCTTCCGAATGTGCCTTTCCACACAGCGCGTTTGCTTCTCCCGGAAAAAGGGAAGA  
TGTTTGCAAAGTTGCCTGGGCCACCCACCTGCCCCGCTTGCCCCCTGCCACCCTCCTACA  
GGTCCTAACTCAGAGAATGGGGCCCCCTCACCATCCCTGAGGAAGGCTCATCGCAGAGAC  
TCAGCCTTCCCATTCTTAAATGGGGAGGAGACCCAGGTTTTCTGCCCATCAGGCAGCC  
AGGAAGATGCAATGAGGCACAGTCATTCTCATCCAGCCAGGCCAGCCCACCTCACTCA  
CCGTATGCAGACTCACCTTGTCCAGGTCATAATAGAAAGCCTGTGA (SEQ ID  
NO:20)

**SNP7**  
**A/G**

CAGCGGCAGAGGCCACTGTGACATACCCAAGATGTGACACCTGACCCACTTTCCTGGCA  
TTACAGAAGCCATCCCAAGTCCAGGTCACCTGATGGCCAAGGTCTATAAAATAGGACCA  
CCTAAAAGAAATGCACCTCCATACTGCCACCTTAGCATTACTTCTAGAACCGAGAG  
ACAGTGTGACATGGGCCTAAAACATGTGAACTGCTGTACGTGCCAAAGTGAAGTTAACT  
CAGTGCAACGTGAAGAGGCTATTCCATAAACCTCTAGTTCTGAGAAAGAGTCACACCGT  
GACATAGGCTAGAAGGAACGCAGGGTTCATCTTTTACTCCTGGCCAAGGCTATCTGGGT  
GGGAAGCAGGCAGGGAGGGGTCTCACCAGCCTGGAATTCCTCCTGGT (SEQ ID  
NO:21)

CAGCGGCAGAGGCCACTGTGACATACCCAAGATGTGACACCTGACCCACTTTCCTGGCA  
TTACAGAAGCCATCCCAAGTCCAGGTCACCTGATGGCCAAGGTCTATAAAATAGGACCA  
CCTAAAAGAAATGCACCTCCATACTGCCACCTTAGCATTACTTCTAGAACCGAGAG  
ACAGTGTGACATGGGCCTAAAACGTGTGAACTGCTGTACGTGCCAAAGTGAAGTTAACT  
CAGTGCAACGTGAAGAGGCTATTCCATAAACCTCTAGTTCTGAGAAAGAGTCACACCGT  
GACATAGGCTAGAAGGAACGCAGGGTTCATCTTTTACTCCTGGCCAAGGCTATCTGGGT  
GGGAAGCAGGCAGGGAGGGGTCTCACCAGCCTGGAATTCCTCCTGGT (SEQ ID  
NO:22)

**SNP8**  
**A/G**

CTCTGCAGTGCGTGCTCCACAAGATCAGAGTCCTCCTGCCTTAGTCACTGCCAGGTTTC  
CAGTGCCCCAAGGACCGGGCTGAGCACGCGGCTGCACCCTGACATACTTGCTTACTAAAC  
GAATGACCAGGAACCTTAACCTGTACCTCTTGTAGACAAGACCCATCCACGCTTCCCCA

**FIG. 4 D**

GGAAGAGACAGAGAGGAGGCGAGATAGAGGAATGCACTTCTTAAAGGCAGCACACAGCC  
CAGCCTTACTTTGAGGCCTCTTTTCAATGCTTCGAAGATCTTCTTCACCTGCTGGGGCTT  
CGGGTCTGCACAGACCGACCCCTTCCGCAGCGTGCCGTACATCTTGGAGGATTTTGCAG  
GCATTCGCGATCTCACGGAGTTCCTGTTGATGGACTTTCTGTGAGAA (SEQ ID  
NO: 23)

CTCTGCAGTGCGTGCTCCACAAGATCAGAGTCCTCCTGCCTTAGTCACTGCCAGGTTTC  
CAGTGCCCAAGGACCGGGCTGAGCACGCGGCTGCACCCTGACATACTTGCTTACTAAAC  
GAATGACCAGGAACCTTAACCTGTCACCTCTTGTAAGACAAGACCCATCCACGCTTCCCCA  
GGAAGAGACAGAGAGGAGGCGAGGTAGAGGAATGCACTTCTTAAAGGCAGCACACAGCC  
CAGCCTTACTTTGAGGCCTCTTTTCAATGCTTCGAAGATCTTCTTCACCTGCTGGGGCTT  
CGGGTCTGCACAGACCGACCCCTTCCGCAGCGTGCCGTACATCTTGGAGGATTTTGCAG  
GCATTCGCGATCTCACGGAGTTCCTGTTGATGGACTTTCTGTGAGAA (SEQ ID  
NO: 24)

**SNP9**  
**A/C**

AGGAACAAACAGAGTCAGACCAAATCTCCATGACAGTGAGTTCCTGGATCTAGCTATGT  
CTAAAGCTGAACCTGCCCCGTGGACTTTGCAGTTACATGAGCCAACTGGCTCTCTTTTTT  
AGCTTAAGCCAGCTGGAGTTGGGAGTGTGGACTGGATGATCCTAAAACTGCCTTTTCAG  
TGGTGATGGCTGGGTCCCTCAACATTTAGAGATGTAGCAGCATCTCAAGACTGATTATA  
GGAGTACGAGGCCAGGGCACCCCTCATCACAGCACAGAGCTGGTTTCCCTGGCATCTAAG  
CCTCTTCTCAGGATCCCATAACTTATCCATGAGGCTGGCTGATGCAGCCTTTGCTCACC  
AACAGATGTGTTGAATTCTGCTCTTAGCCCTCTAAAGCCATCAGCCA (SEQ ID  
NO: 25)

AGGAACAAACAGAGTCAGACCAAATCTCCATGACAGTGAGTTCCTGGATCTAGCTATGT  
CTAAAGCTGAACCTGCCCCGTGGACTTTGCAGTTACATGAGCCAACTGGCTCTCTTTTTT  
AGCTTAAGCCAGCTGGAGTTGGGAGTGTGGACTGGATGATCCTAAAACTGCCTTTTCAG  
TGGTGATGGCTGGGTCCCTCAACCTTTAGAGATGTAGCAGCATCTCAAGACTGATTATA  
GGAGTACGAGGCCAGGGCACCCCTCATCACAGCACAGAGCTGGTTTCCCTGGCATCTAAG  
CCTCTTCTCAGGATCCCATAACTTATCCATGAGGCTGGCTGATGCAGCCTTTGCTCACC  
AACAGATGTGTTGAATTCTGCTCTTAGCCCTCTAAAGCCATCAGCCA (SEQ ID  
NO: 26)

**FIG. 4 E**

**SNP10**

**C/T**

TCTTGGGGCATCAACTTAAACCCCTTCCCAGGCTCCCCTCCACTGAGAATGTGTCTCAAG  
GCCTCACTGCAGCCCATGAGGCTCCGCAGGGTCCTCCTCCCTCCCTGACTGCTGTACG  
CATGCCAGCCGCACACCTGCTTTCTGTCCCTTAAAGCTCATTCCCACCCAGGACATCTG  
CACTCGCAGCTGCCTCCCGCCGCGAAGGCTTCCCGGCCACCCCCATCTGCACACGCG  
CAGATCCACTTCTTCTGTCCCTTCCTGCCTCCACTCCCCATGCCCCTGTCTCGTCAGGC  
TCTCCCAGGAGACCATGGGTGCCCTCCCCACCCCCAGTTCAGTTCCCTCACAGCACTG  
CCACCAGCTGGATCTGTCTCAATTATCACTGGCTTATTGTTTGCTGC (SEQ ID  
NO: 27)

TCTTGGGGCATCAACTTAAACCCCTTCCCAGGCTCCCCTCCACTGAGAATGTGTCTCAAG  
GCCTCACTGCAGCCCATGAGGCTCCGCAGGGTCCTCCTCCCTCCCTGACTGCTGTACG  
CATGCCAGCCGCACACCTGCTTTCTGTCCCTTAAAGCTCATTCCCACCCAGGACATCTG  
CACTCGCAGCTGCCTCCCGCCGCGAAGGCTTCCCGGCCACCCCCATCTGCACACGCG  
CAGATCCACTTCTTCTGTCCCTTCCTGCCTCCACTCCCCATGCCCCTGTCTCGTCAGGC  
TCTCCCAGGAGACCATGGGTGCCCTCCCCACCCCCAGTTCAGTTCCCTCACAGCACTG  
CCACCAGCTGGATCTGTCTCAATTATCACTGGCTTATTGTTTGCTGC (SEQ ID  
NO: 28)

**SNP11**

**C/T**

GTTTCTGTCTGCTGGTTGTTAAACACGTATGAGCTCCTCACTGCTGTTACCCCTATCAG  
CACCTATGCAGGGCCTGAGAAGCTGCTCAAAGCTGCTTGATCCCCCAGCCAAGCCAGGC  
AAGAGAATAAGGACGGAGTAGGGAGGGATTCCCAAAGGTGAGTAGTTGAGACGTACTCC  
GGAGCCAGCCTGGGCACTGGAGCGGGAAGGGGCTTCCCCGGCCCCCTCCCTCTGCACCTT  
CCCATCAGAAGCCTTCTGGGCCGTTTCCTGGAGCTTCACCCCAGTCACTCCACTTCAAGG  
TCAGAGAGAAGGACAATTGCTAAGCAGTTCCTCCCGATGCAAAGCTCAAACAAGCCCC  
AGGTCCTCCTGCTCAGTGTGAGAGAGAGGACGACGAAGGAGGGAAAC (SEQ ID  
NO: 29)

GTTTCTGTCTGCTGGTTGTTAAACACGTATGAGCTCCTCACTGCTGTTACCCCTATCAG  
CACCTATGCAGGGCCTGAGAAGCTGCTCAAAGCTGCTTGATCCCCCAGCCAAGCCAGGC  
AAGAGAATAAGGACGGAGTAGGGAGGGATTCCCAAAGGTGAGTAGTTGAGACGTACTCC  
GGAGCCAGCCTGGGCACTGGAGCGGGAAGGGGCTTCCCCGGCCCCCTCCCTCTGCACCTT  
CCCATCAGAAGCCTTCTGGGCCGTTTCCTGGAGCTTCACCCCAGTCACTCCACTTCAAGG  
TCAGAGAGAAGGACAATTGCTAAGCAGTTCCTCCCGATGCAAAGCTCAAACAAGCCCC

**FIG. 4 F**

AGGTCCTCCTGCTCAGTGTGAGAGAGAGGACGACGAAGGAGGGAAAC (SEQ ID  
NO:30)

**SNP12**

**G/A**

CCAAGGTGTGGCTGGAGGAAGCAGAGTCTACTCCCGCTAAGTCTGTCCGCTCACTGCTG  
GCCAAAGCTGCCCTGCGTCTCCTCCCCACCGCCAGCCAGAGGGAACCTGCAATTTACCC  
TCATTTAGAGGTAAAACATCTAAATTTAACGTTATGGGCTTTTGGGGCTGGGTGGCTTT  
TATGCCTGAGTCCCTCACTTAGGGCTCCTTTTTATCCACTCAAATGCCAGCTAGGGCTT  
AGTTTGTATTATAGGAGTTTCCAAAATAGCTCCTTTGGTTTCGCATGAAAGGAAATGGCA  
AAATAGCCCAGGAAGAGGAATGTGAGTTTACACAGAAGACAGACAGGCGCCCGAGGAGG  
CTTCTCTGGGAACCAAGTTCGCCTGTACCAGAGGGGGCCCGAGAAAGT (SEQ ID  
NO:31)

CCAAGGTGTGGCTGGAGGAAGCAGAGTCTACTCCCGCTAAGTCTGTCCGCTCACTGCTG  
GCCAAAGCTGCCCTGCGTCTCCTCCCCACCGCCAGCCAGAGGGAACCTGCAATTTACCC  
TCATTTAGAGGTAAAACATCTAAATTTAACGTTATGGGCTTTTGGGGCTGGGTGGCTTT  
TATGCCTGAGTCCCTCACTTAGGACTCCTTTTTATCCACTCAAATGCCAGCTAGGGCTT  
AGTTTGTATTATAGGAGTTTCCAAAATAGCTCCTTTGGTTTCGCATGAAAGGAAATGGCA  
AAATAGCCCAGGAAGAGGAATGTGAGTTTACACAGAAGACAGACAGGCGCCCGAGGAGG  
CTTCTCTGGGAACCAAGTTCGCCTGTACCAGAGGGGGCCCGAGAAAGT (SEQ ID  
NO:32)

**SNP13**

**G/C**

TACGTTAGAAGGACCCTACGTTAGAAGGGTGAGGCGCTAGGGCCATAGCCTAAGGGCAC  
TGGGAACCCTGTGGGCATGCGCAGTTCAAGCCCATCCCCGCTCCCTCCAGCTGCTGTCC  
ATCCCTGCCACACCTGACCATTTGCCTAACCTAGATCCTTCCTGTCTTGCAATTCCTCA  
AGCATCCGGAGCCCAGGACTGCTGAGTCAACCCTCTGGAATGCCCACTCCCCACAG  
GCCAGCCGGCCTTGGGACTCCCGCACAGCCACGTGAGCCGGTGGAGCCGGGTCTGTTTG  
CTAGTGGAGGCTGTAAACAGCACGGGAAGTGGTCAAGGGTTCAACAAGAGATGAGCCAT  
CTGGTCCTCCAGAGGTAAACAATTTACAAGAGACACATCAAGCCGGC (SEQ ID  
NO:33)

TACGTTAGAAGGACCCTACGTTAGAAGGGTGAGGCGCTAGGGCCATAGCCTAAGGGCAC  
TGGGAACCCTGTGGGCATGCGCAGTTCAAGCCCATCCCCGCTCCCTCCAGCTGCTGTCC  
ATCCCTGCCACACCTGACCATTTGCCTAACCTAGATCCTTCCTGTCTTGCAATTCCTCA

**FIG. 4 G**

AGCATCCGGAGCCCAGGACTGCTCAGTCAACCCCTCTGGAATGCCCACAACCTCCCCACAG  
GCCAGCCGGCCTTGGGACTCCCGCACAGCCACGTGAGCCGGTGGAGCCGGGTCTGTTTG  
CTAGTGGAGGCTGTAAACAGCACGGGAAGTGGTCAAGGGTTCAACAAGAGATGAGCCAT  
CTGGTCCTCCAGAGGTAAACAATTTACAAGAGACACATCAAGCCGGC (SEQ ID  
NO: 34)

**SNP14**  
**C/T**

GGGTTTCCCCCAAGCCCCTTTCCCCCTTTGCGCCTCCCACTTCTCCTAGATTGAGAGTC  
AGCTTG GTTCTTTCTTTACATCCATTAGTGAGGGTCAGGCTCTTTTGTTATGTTTTTT  
TTTCTTTTGTATAACTTAATTATTTAGGGTTCGGGGTGGGCGCTCGCCCCTTGCCCAG  
TCACACTGGTGTGTGTGCGACTCTTACAAAGTTAACAGTTTCTCCAGGTCAAGGGGTGG  
GATCCAGGCTTGGTGATGTGCACAATTTCTTTTGTCCACTTGACACATCTCTGCGTCCT  
GATTCTGCTCAGGGACGGACCCAAGAACAAGCAGCCATTTACCGCCTCCGGAGGGGAG  
GCCAGCCCTGTGGCACATCCAGGGCCTTGGAACACCTAGAGACAGAT (SEQ ID  
NO: 35)

GGGTTTCCCCCAAGCCCCTTTCCCCCTTTGCGCCTCCCACTTCTCCTAGATTGAGAGTC  
AGCTTG GTTCTTTCTTTACATCCATTAGTGAGGGTCAGGCTCTTTTGTTATGTTTTTT  
TTTCTTTTGTATAACTTAATTATTTAGGGTTCGGGGTGGGCGCTCGCCCCTTGCCCAG  
TCACACTGGTGTGTGTGCGACTCTTACAAAGTTAACAGTTTCTCCAGGTCAAGGGGTGG  
GATCCAGGCTTGGTGATGTGCACAATTTCTTTTGTCCACTTGACACATCTCTGCGTCCT  
GATTCTGCTCAGGGACGGACCCAAGAACAAGCAGCCATTTACCGCCTCCGGAGGGGAG  
GCCAGCCCTGTGGCACATCCAGGGCCTTGGAACACCTAGAGACAGAT (SEQ ID  
NO: 36)

**FIG. 4 H**



SNP Table

SNP Name	Source	dbSNP ID	Nucleotide Change	Position
SNP1	dbSNP	rs16437	TTGA IN/DEL	48931488
SNP2	dbSNP	rs1060402	A/G	48933573
SNP3	Joslin		A/G	48940121
SNP4	Joslin		A/G	48942634
SNP5	Joslin		A/C	48954431
SNP6	Joslin		TTAGTGCCGGGCCGGC (SEQ ID NO: 8) IN/DEL	48956026
SNP7	dbSNP	rs2426169	A/G	48960837
SNP8	Joslin		A/G	48964956
SNP9	dbSNP	rs768175	A/C	48966905
SNP10	Joslin		C/T	48973501
SNP11	dbSNP	rs2426183	C/T	48978623
SNP12	Joslin		A/G	48981954
SNP13	Joslin		G/C	48990734
SNP14	Joslin		C/T	49037219

\*Genomic positions correspond to the Build 29 human genome assembly from NCBI (UCSC version hg11)

**FIG. 5**

**FIG. 6A**

```

361 WLHPSDPKPRRLSVLSALQDTFFAKLHRSRFSFSLPSLRSPKAVLELYSNLPDDIFENG 420
    |||||
360 .....SNLPDDIFENG 370

    . . . . .
421 KAAEEKMPLSLSFSDLPNGDCALTSHSTGSPSNSTNPEITITPAEFNLSLASQNEGMDD 480
    |||||
371 KAAEEKMPLSLSFSDLPNGDCALTSHSTGSPSNSTNPEITITPAEFNLSLASQNEGMDD 430

    . . . . .
481 TSSASSRNSLGEQEPKSHLKEEDPEEPRKPASAPSEACRRQSSGAGAEHLFLENDVAEA 540
    |||||
431 TSSASSRNSLGEQEPKSHLKEEDPEEPRKPASAPSEACRRQSSGAGAEHLFLENDVAEA 490

    . . . . .
541 LLQSEEEASELKPVELDTSEGNITKQLVKRLTSAEVPMATDRLLSEGSVGGESEGCRSFL 600
    |||||
491 LLQSEEEASELKPVELDTSEGNITKQLVKRLTSAEVPMATDRLLSEGSVGGESEGCRSFL 550

    . . . . .
601 DGSLEDAFNGLLLALEPHKEQYKEFQDLNQEVNLDLILKCKPAVSRSRSSSLTVEA 660
    |||||
551 DGSLEDAFNGLLLALEPHKEQYKEFQDLNQEVNLDLILKK..... 591

661 LESFDFLNTSDFDEEEDGDEVCVNGGADSVFSDTETEKHSYRSVHPEARGHLSEALTED 720

721 TGVGTSVAGSPPLTTGNESLDITIVRHLQYCTQLVQQIVFSSKTPFVARSLLEKLSRQI 780

781 QVMEKLAADVSDENIGNISSVVEAIPFEFHKKLLSLSFWTKCCSPVGVIHSPADRVMMKQLEA 840

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**FIG. 6B**

841 SFARTVNKEYPGLADPVFRTLVSQILDQAEPLLSSSLSSEVVTVFQYYSYFTSHGVSDLE 900  
901 SYLSQLARQVSMVQTLLQSLRDEKLLQTMSDLAPSNLLAQQEVLRTLALLLTREDNEVSEA 960  
961 VTLYLAAASKNQHFREKALLYCEALTKTNLQLQKAAACLALKILEATESIKMLVTLCQSD 1020  
1021 TEEIRNVASETLLSLGEDGRLAYEQLDKFFPRDCVKVGRHGTAVATAF 1068  
Top sequence: predicted Diff40 long form (BAA20840) (SEQ ID NO:23)  
Bottom sequence: predicted Diff40 short form NCBI (NP\_056948) (SEQ ID NO:24)

**FIG. 6C**



```

358 FFRWL.HPSPDK.....PRRLSVLSALQDTFFAKLHRRSRFSDL..PSLRSPKAVLELY 409
   : | | . | | | | | | | | | | | | | | | | | | | | | | | | | | | |
357 YLSVLQQPTQQALLLGGPRATSILSYLSD.....SDLRGPSLR..... 394

410 SNLPDDIFENGKAAEEKMPLSLSFSDLPNGDCALTSHTGSPSNSTNPEITITPAEFNLS 469
   . :.: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
395 .....SQSQELPEMDSFSSSEDPRD...TETST...SASTS.DVGFLPLTFG.. 433

470 SLASQNEGMDDTSSASSRNSLGEQGEPKSHLKEEDPEEPRKPASAPSEACRRQSSGAGAE 529
   | . :.: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
434 .....PHASIEEEAREDP LLPGLPEMA..HLSGGPF AE 465

530 HLFLENDVAEALLQEESEASELKPVVELDTSEGNITKQLVKRLTSAEVPMATDRLLSEGSV 589
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
466 QPGWRN.....LGGES.....P...SLPQGS.....LFHSGTASSSQNGHEEGAT 502

590 GGESEGCRSFLDGSLEDAFNGLLLALEPHKEQYKEFQDLNQEVNMNLDLILKCKPAVRSR 649
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
503 GDREDGPGVALEGPLQE...VLELLRPTDSTQPQLRELEYQVLGFRDRLK..PCRARQE 556

650 SSSLSLTVESALESFDFLNTSDFDEEEDGDEVNCNVGGGADSVFSDTETEKHSYRSVHPEA 709
   . | . | | | | | | | | | | | | | | | | | | | | | | | | | | | |
557 HTSAESLMECILESFAFLN.ADFALDE.....LSLEFGGSQGLRKD.....RPLPPP. 601

```

FIG. 7B

```

710 RGHLSALETDTGVGTSVAGSPPLTTGNESLDITIVRHLQYCTQLVQQIVFSSKTPFVA 769
    .|. | || | ||: :: ||| | |.|.: . . |
602 .....SSLKASSRELTAGAPELDVLLMVHLQVCKALLQKLASPNLSRLVQ 646

770 RSLLEKLSRQIQVMEKLAASVDENIGNISSVVEAIPFHKKLSLLSFWTKCCSPVGVYHS 829
    |||. . | :| |. . | :| |. | :| | | | |
647 ECLLEEVAQQKHVLETLVLDFEKVKGATSIIEIIPQASRTKGCCLKLWRGCTGPGRVLS 706
    . 7
830 PADRMKQLEASFARTVNKEYPGLADPVFRTLVSQILDQAEPLSSSSLSSE.VVTVFQYY 888
    || :| |. . | .||| :| |. |. |. | :| | :| |
707 PATLLNQLKKTFQHRVRGKYPGQLEIACRRILLEQVSCGGLPGAGLPEEQIITWFOFH 766

889 SYFTSHGVSDLESYLSQARQVSMVQTLQSLRDEKLLQTMSDLAPSNLLAQQEVLRTLAL 948
    || |||| :| | :| | :| | :| | :| | :| | :| |
767 SYLQRQSVSDLEKHFTQLTKEVTLIEELHCAGQAKVVRKLGQKRLGQLPLPQTLRAWAL 826

949 LLTREDNEVSEAVTLYLAAASKNQHFREKALLYCEALTKTNLQLQKAACLALKILEATE 1008
    | | | . || | :| | :| | :| | :| | :| | :| | :| |
827 LQLDGTPRVCRAASARLAGAVRNRSFREKALLFYTNALAENDARLQQAACLALKHLKGIE 886

1009 SIKMLVTLCQSDTEEIRNVASETLLSLGEDGRLAYEQDK 1048
    || .||| | :| | | | | | | | | | :| |
887 SIDQTASLCQSDLEAVRAAAARETTLSFGEKGRLAFAEKMDKLCSEQREVCQADVEITIF 946

```

Top sequence: predicted Diff40 long form (BAA20840) (SEQ ID NO:23)  
 Bottom sequence: T2DM-1a (SEQ ID NO:2)

**FIG. 7C**

```

1 MLVGSQSFSPG..GPNGLI.RSQSFAGFSGLQERRSRCNSFIENSALKKPQAKLKKMHN 57
  | | . | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MSVRLRFLSPGDTGAVGVVGRSASFAGFSSAQSRRI.AKSINRNSVRSRMP.AKSSKMYG 58
  . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
58 LGHKNNPPKEPQPKRVEEVYALKNGLDEYLEVHQTELDKLTAQLKDMKRNSRLGVLYD 117
  | . :|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.
59 TLRK.GSVCADPKPQQVKKIFEALKRGLKEYLCVQQAELDHLSGRHKDTRRNSRLAFYYD 117
  . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
118 LDKQIKTIERYMRRLEFFHISKVDLEYEAYCQRRQLQDGASKMKQAFATSPASKAARESLT 177
  | | | :| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
118 LDKQTRCVERHIRKMEFHISKVDLEYEDYCIQCRLRDGASSMQRAFAFCPPSRAARESLQ 177
  . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
178 EINRSFKEYTENMCTIEVELENLLGEFSIKMKGLAGFARLCPGDQYEIFMKYGRQRWKLK 237
  |:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
178 ELGRSLHECAEDMWLIEGALEVLHGEFHIRMKGLVGYARLCPGDHYEVLMLRQLGRWKLK 237
  . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
238 GKIEVNGKQSWDGEETVFLPLIVGFISIKVTELKGLATHILVGSVTCETKELFAARPQVV 297
  |:| | . |.| | | | | | | | | | | | | | | | | | | | | | | | | |
238 GRIESDDSQTWDEEEKAFIPTLHENLDIKVTELRLGLS.LAVGAVTCADIADFFTRPQVI 296
  . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
298 AVDINDLGTIKLNLEITWYPFDVEDMTASSGAGNKAAALQRRMSMYSQGTPTPTFKDHS 357
  | | | :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
297 VVDITELGTIKLQLEVQWNPFDTESFLVSPSPTGKFSMGSRKGSLYNWTTPPSTPSFRERY 356
  
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**FIG. 8A**



Top sequence: predicted Diff40 Short form (RefSeq NP\_056948) (SEQ ID NO:24)  
Bottom sequence: T2DM-1b (SEQ ID NO:4)

**FIG. 8B**

>T2DM1 and T2DM2 refseq, +/-1000bp

GCCTGAGGCCACCCTCCAAGTGTCCCCACAGCGCACCACAAGACCACAGGAGTGACCTCC  
TCACTGGCAGGTATTTGGGGAAACAACCTGCTGTCTACTCTTTTGGGTAAAAAGTGAAACA  
CCAATAGTTTAAATTGAAATTTTCAGAAAATTGAACATATGAACAAGGCAAATAAATACTAA  
GTAAGTTAAAAACACAAAATATGTCCAGGAAGTATCGATGAGAAATGTTCAAGTTAAAGTT  
CTCCAATGCCATTGCTACAGCAACCTCAAACCCTAGGTTCTCTCTGCACTATTAACACAG  
ACATCTCAGGACATGGTTTGCTTTTTTTTTTAAGACTTAAATAGGAAACTAATTTTTCTTTC  
TTTAAAGCAATTGCGTTCTTCAGTGAACCTCTTCTTTAGGCCAGTTGATGGCTTCTTAGC  
AGTTTATTGACGAGATCCTAGGGTAGCTTCCGAAGCTGGGTTGATTGATTGCATTTGGGT  
GCGGATGGCCAAAGTGAGTGGCCCTACTGCCTGTGCTGCTCAGGGCTCCTGGGCTGATGT  
GGTGGCTTCTTCCCTTTGTGCTGCTGAACATAGGGAAAGTGAGGTTACACAGTCCACCATC  
CACCAGCCGCCGTCTGTGAGCTCCACCAGCACTCGCAGCAAGTCAGTCGGGCTGAGAGTG  
TGGTTGTAGAAACCCTGGCTTTGTGCCTTCCCACCTTCCCCAGCTCACCAAGGTGACACC  
TGGCTGCTGCTGAAATGGCCTGAGCAGTCTTGCAATTAGCAGGGCCAGCCACCTGCCAGCC  
TGCTGCATCCCCAGTGCTTCTTGACGCAGAAGTGCCGAGCAGCTGACCGGCAGCGAGGCC  
TGGAGTTCTACACACTTGCCTTGAGGCCTTTTATTTAGGGCCTCAACTTGCCTGGCCTTG  
GCCCTTTTGTAGGTGGCCACCTAGTTTGGCTCAGCTCTGCATCTCGGGGAAGGTCACACA  
GACCCTCAGCCAGAAGTTGAGCGCTCTGTTGAGGCCGTGCAGCCCCTGGAATGCTGTACC  
TTTGCCTTGCTTTTTTCTGCCTCTGTACAAAAGACCAGCCCATGCCCTGGGGCTGGGTCA  
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CATTACCCAGAGTGCAGGCTATGTCCAGGCTGGGCAGCAGCAAAAAAACGATGTGAGAT  
TTGTGCTCATCAGCCAGGATTTTTTAAATATTGTGATTTCAACATCTGCCTCCTGGCAA  
AAGACTTCTCTTTGTTCTGAGCAGAGCTTGTCATCTTCTCAAAAGCTAACCGTCCTTTT  
TCACCTGAAATAGCAAAGGGACCTGTGAGCGGGTTGGATCCTGCCTTGGCACTTCCAAC  
CTCCTGGGCCAGGGTGGCCCTAGTGCTTAGTGACTGTGGGTCTCAGTGGTCTCTGCAAAG  
CGGCAGGGGAGGGAGTATGTGCGGGAGCCCCACCTGGTGACTCACATGGCCTGGGGGCC  
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CTTGGCAGGATGCTACAAAGGGTGGAGGTCGGCTCTGTGCCAGGGCTGCTAACGGTGCCC  
ATCCCAGGTGCCCCAGAGTTGTTCTGCCTGCTGGGAGAGCTGGGTGTGGCCTCTCGCAGA  
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CAGTGTGGTTTCCCGGGCTGCCGCCCGCACGGCCTCCAGGTCAGACTGGCACAGGCTGGC  
AGTCTGGTCGATGCTTTCAATGCCCTGTTTCGAGATTAGGAGAAAAAGAACCCTTTAGGGG  
GCCTTCTCAACAGCAGGTAGAGTCCACTTAGTGGCCCTGCAGGGCCAGTCCTAGCATGGT  
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GGGCCTAACTTGACTCAGCTGAAAACAAAGCTGGCACTTGCTTCATGTGTTATTGTAGGG  
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- FIG.9R -

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GGGAATTCCATGCTGGCCCCCAGCAGGCGGGGCCCCCACCCTTCACGTCCCACCCCCCA  
CTCCCATTTTGGCAAGGGGACTGGGAAAAGGCAGCTAATTTCAAGTCCGCACAGCGTTTG  
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GCTAATCACAAACAGACTGGGACGCAGCCTACCCCTCCTAAACTGCTCTTGGCCACCCCC  
TCCCTCCTCCAGCCCTCTCCTTCTTCTTACCTTGTCACTTTCCTCCAGCCCCCTTCT  
CACTCTTTCTCCTTTCCCTCCTTTCTTTCCCCTTTCCCATCTGTCCGCCTCTTCAGTCCA  
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CTTTGCGCCTCCCATTCTCCTAGATTGAGAGTCAGCTTGGTTCTTTCTTTTACATCCAT  
TAGTGAGGGTCAGGCTCTTTTGTTATGTTTTTTTTTCTTTTGTATAACTTAATTATTTCA  
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GCACACACACAGACTCTGAAGGGTAATTTGGCAAAGACCTCTGAAAACCAGAGATGAGGG  
TCTCCTACTACTTATGCCTGTGCACAGGAGACAGGCACAGAGATGCTTGCTGAGAGCTGC  
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AGATGTGAAAGATATGGTACATCAGGC



T2DM1 and T2DM2 reference sequence and SNP position

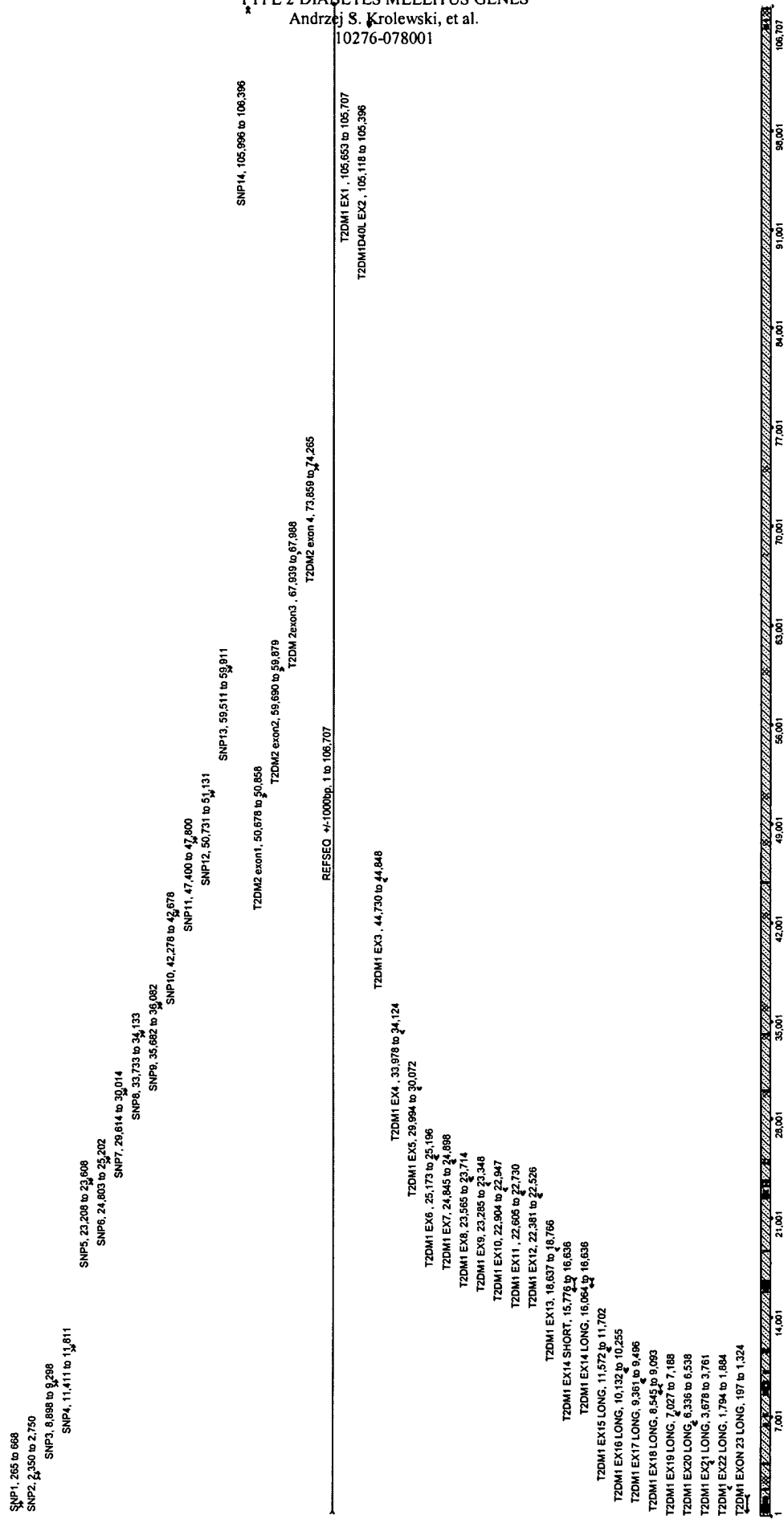


FIG. 10